<110> Wang, Yan
      Xi, Lei
      Prosen, Dennis E.
      MJ Bioworks, Inc.

<120> Improved Nucleic Acid Modifying Enzymes

<130> 020130-000111US

<140> US 09/870,353
<141> 2001-05-30

<150> US 60/207,567
<151> 2000-05-26

<150> US 09/640,958
<151> 2000-08-16

<160> 34

<170> PatentIn Ver. 2.1

<210> 1
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      sequence non-specific double-stranded nucleic acid
      binding protein Ssod7d

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<222> (1)..(189)
<223> Ssod7d

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<211> 63
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<213> Artificial Sequence

<220>
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      sequence non-specific double-stranded nucleic acid
      binding protein Ssod7d

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Ser Lys Ile Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr
      20   25   30

Tyr Asp Glu Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys
          35   40   45
Asp Ala Pro Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
        50   55   60

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<211> 1899
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
      Ssod7d-deltaTaq

<220>
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<222> (1)..(1899)
<223> Ssod7d-deltaTaq

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gagggcggtg gcaagaccgg ccgtggtgcg gtaagcgaaa aggacgcgcc gaaggagctg 180
ctgcagatgc tggagaagca gaaaaagggc ggcggtgtca ctagtcccaa ggccctggag 240
gaggcccccct ggcccccgcc ggaaggggcc ttcgtgggct ttgtgctttc ccgcaaggag 300
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cccgagcctt ataaagccct cagggacctg aaggaggcgc ggggcttct cgccaaagac 420
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<220>
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      Ssod7d-deltaTaq

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Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly Gly Gly Lys Thr Gly Arg
        35                  40                  45
Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu
    50                  55                  60
Glu Lys Gln Lys Lys Gly Gly Gly Val Thr Ser Pro Lys Ala Leu Glu
65                  70                  75                  80
Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu
                85                  90                  95
Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala Ala
            100                 105                 110
Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg
        115                 120                 125
Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu
    130                 135                 140
Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu
145                 150                 155                 160
Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
                165                 170                 175
Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala
            180                 185                 190
Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu
            195                 200                 205
Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala
    210                 215                 220
Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
225                 230                 235                 240
Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu
            245                 250                 255
Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
            260                 265                 270
Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile
    275                 280                 285
Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
    290                 295                 300
Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr
305                 310                 315                 320
Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp
            325                 330                 335
Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
            340                 345                 350
Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
    355                 360                 365
Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile
    370                 375                 380
Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
385                 390                 395                 400
Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
            405                 410                 415
Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe
            420                 425                 430
Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
        435                 440                 445
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3

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Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
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Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg
465                 470                 475                 480
Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
                485                 490                 495
Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
                500                 505                 510
Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala
            515                 520                 525
Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
        530                 535                 540
Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met
545                 550                 555                 560
Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu Ala
                565                 570                 575
Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met
            580                 585                 590
Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile
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Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly Ile Asp Gly Arg Gly Gly
    610                 615                 620
Gly Gly His His His His His His
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<210> 5
<211> 2763
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
      Ssod7d/full-length Taq

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<221> CDS
<222> (1)..(2763)
<223> Ssod7d/full-length Taq

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gagggcggtg gcaagaccgg ccgtggtgcg gtaagcgaaa aggacgcgcc gaaggagctg 180
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<211> 920
<212> PRT
<213> Artificial Sequence

<220>
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     Ssod7d/full-length Taq

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            20                  25                  30
Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly Gly Gly Lys Thr Gly Arg
        35                  40                  45
Gly Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Gln Met Leu
    50                  55                  60
Glu Lys Gln Lys Lys Gly Gly Gly Val Thr Ser Gly Met Leu Pro Leu
65                  70                  75                  80
Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly His His Leu Ala
                85                  90                  95
Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr Ser Arg Gly Glu
            100                 105                 110
Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu Leu Lys Ala Leu
        115                 120                 125
Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp Ala Lys Ala Pro
    130                 135                 140
Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala Gly Arg Ala Pro
145                 150                 155                 160
Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile Lys Glu Leu Val
                165                 170                 175
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Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp
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        195                     200                 205
Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln Leu Leu Ser Asp
    210                 215                 220
Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile Thr Pro Ala Trp
225                 230                 235                 240
Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp Ala Asp Tyr Arg
            245                 250                 255
Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly Val Lys Gly Ile
            260                 265                 270
Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser Leu Glu
            275                 280                 285
Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg Glu Lys
    290                 295                 300
Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp Asp Leu Ala Lys
305                 310                 315                 320
Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala Lys Arg Arg Glu
                325                 330                 335
Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly
            340                 345                 350
Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Lys Ala Leu Glu
        355                 360                 365
Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu
    370                 375                 380
Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala Ala Ala
385                 390                 395                 400
Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala Leu Arg
                405                 410                 415
Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser Val Leu
            420                 425                 430
Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro Met Leu
        435                 440                 445
Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala
    450                 455                 460
Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Ala
465                 470                 475                 480
Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu Gly Glu
            485                 490                 495
Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu Ser Ala
        500                 505                 510
Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr
        515                 520                 525
Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg Leu Glu
    530                 535                 540
Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg
545                 550                 555                 560
Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro Ala Ile
            565                 570                 575
Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu
            580                 585                 590
Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln Tyr
        595                 600                 605
Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu Pro Asp
    610                 615                 620
Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr
625                 630                 635                 640
Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn
            645                 650                 655
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6

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Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Ile
        660                     665                 670
Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu
        675                     680                 685
Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val
        690                     695                 700
Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp Met Phe
705                     710                 715                 720
Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys
                725                 730                 735
Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser
                740                 745                 750
Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile Glu Arg
        755                     760                 765
Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu
        770                     775                 780
Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg
785                     790                 795                 800
Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg Glu Ala
                805                 810                 815
Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp
                820                 825                 830
Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu Glu Met
        835                     840                 845
Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu Glu Ala
        850                     855                 860
Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu Val Met
865                     870                 875                 880
Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Ile
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Gly Gly His His His His His His
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<212> DNA
<213> Artificial Sequence

<220>
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     Pfu-Ssod7d

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<223> Pfu-Ssod7d

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aagattgtga gaattgttga tgtagagaag gttgagaaaa agtttctcgg caagcctatt 240
accgtgtgga aactttattt ggaacatccc caagatgttc ccactattag agaaaaagtt 300
agagaacatc cagcagttgt ggacatcttc gaatacgata ttccatttgc aaagagatac 360
ctcatcgaca aaggcctaat accaatggag ggggaagaag agctaaagat tcttgccttc 420
gatatagaaa ccctctatca cgaaggagaa gagtttggaa aaggcccaat tataatgatt 480
agttatgcag atgaaaatga agcaaaggtg attacttgga aaaacataga tcttccatac 540
gttgaggttg tatcaagcga gagagagatg ataaagagat tctcaggat tatcagggag 600
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atgcagagaa taggcgatat gacggctgta gaagtcaagg gaagaataca tttcgacttg 780
tatcatgtaa taacaaggac aataaatctc ccaacataca cactagaggc tgtatatgaa 840
gcaatttttg gaaagccaaa ggagaaggta tacgccgacg agatagcaaa agcctgggaa 900
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gctctagaat ttgtaaaata cataaattca aagctccctg gactgctaga gcttgaatat 1740
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ctcgcaatat atgagcagat aacaagacca ttacatgagt ataaggcgat aggtcctcac 2040
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aagaaagtat ggcgtgtggg caagatgatc tccttcacct acgacgaggg cggtggcaag 2460
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<210> 8
<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
     Pfu-Ssod7d

```
<400> 8
Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile
1               5                   10                  15
Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg
            20                  25                  30
Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile
        35                  40                  45
Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg
    50                  55                  60
Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile
65                  70                  75                  80
Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile
                85                  90                  95
Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr
            100                 105                 110
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro
        115                 120                 125
```

```
Met Glu Gly Glu Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr
    130             135             140
Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile
145             150             155             160
Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile
            165             170             175
Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
            180             185             190
Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr
    195             200             205
Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu
    210             215             220
Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys
225             230             235             240
Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile
            245             250             255
His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr
            260             265             270
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu
    275             280             285
Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn
    290             295             300
Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr
305             310             315             320
Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu
            325             330             335
Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
            340             345             350
Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala
    355             360             365
Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser
    370             375             380
Tyr Thr Gly Gly Phe Val Lys Glu Pro Glu Lys Gly Leu Trp Glu Asn
385             390             395             400
Ile Val Tyr Leu Asp Phe Arg Ala Leu Tyr Pro Ser Ile Ile Ile Thr
            405             410             415
His Asn Val Ser Pro Asp Thr Leu Asn Leu Glu Gly Cys Lys Asn Tyr
            420             425             430
Asp Ile Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Ile Pro Gly
    435             440             445
Phe Ile Pro Ser Leu Leu Gly His Leu Leu Glu Glu Arg Gln Lys Ile
    450             455             460
Lys Thr Lys Met Lys Glu Thr Gln Asp Pro Ile Glu Lys Ile Leu Leu
465             470             475             480
Asp Tyr Arg Gln Lys Ala Ile Lys Leu Leu Ala Asn Ser Phe Tyr Gly
            485             490             495
Tyr Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu
            500             505             510
Ser Val Thr Ala Trp Gly Arg Lys Tyr Ile Glu Leu Val Trp Lys Glu
    515             520             525
Leu Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ile Asp Thr Asp Gly
    530             535             540
Leu Tyr Ala Thr Ile Pro Gly Gly Glu Ser Glu Glu Ile Lys Lys Lys
545             550             555             560
Ala Leu Glu Phe Val Lys Tyr Ile Asn Ser Lys Leu Pro Gly Leu Leu
            565             570             575
Glu Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys
            580             585             590
Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly
    595             600             605
```

```
Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln
    610                 615                 620
Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala
625                 630                 635                 640
Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile
                645                 650                 655
Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His
                660                 665                 670
Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala
        675                 680                 685
Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val
        690                 695                 700
Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu
705                 710                 715                 720
Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn
                725                 730                 735
Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg
                740                 745                 750
Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser
                755                 760                 765
Trp Leu Asn Ile Lys Lys Ser Gly Thr Gly Gly Gly Gly Ala Thr Val
        770                 775                 780
Lys Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile
785                 790                 795                 800
Lys Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu
                805                 810                 815
Gly Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro
                820                 825                 830
Lys Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys
        835                 840
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<210> 9
<211> 1904
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
     Sac7d-deltaTaq

<220>
<221> CDS
<222> (1)..(1904)
<223> Sac7d-deltaTaq

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<400> 9
atgattacga attcgacggt gaaggtaaag ttcaagtata agggtgaaga gaaagaagta 60
gacacttcaa agataaagaa ggtttggaga gtaggcaaaa tggtgtcctt tacctatgac 120
gacaatggta agacaggtag aggagctgta agcgagaaag atgctccaaa agaattatta 180
gacatgttag caagagcaga aagagagaag aaaggcggcg tgtcactag tcccaaggcc 240
ctggaggagg cccctggcc cccgccggaa ggggccttcg tgggctttgt gctttcccgc 300
aaggagccca tgtgggccga tcttctggcc ctggccgccg caggggggg ccgggtccac 360
cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc 420
aaagacctga gcgttctggc cctgagggaa ggccttggcc tcccgcccgg cgacgacccc 480
atgctcctcg cctacctcct ggacccttcc aacaccaccc ccgaggggt ggcccggcgc 540
tacggcgggg agtggacgga ggaggcgggg gagcgggccg cccttccga gaggctcttc 600
gccaacctgt ggggggaggct tgaggggag gagaggctcc tttggcttta ccgggaggtg 660
gagaggcccc tttccgctgt cctggcccac atggaggcca cgggggtgcg cctggacgtg 720
gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccggg 780
tcttccgcct ggccggccac cccttcaacc tcaactcccg ggaccagctg gaaagggtcc 840
```

```
tctttgacga gctagggctt cccgccatcg gcaagacgga gaagaccggc aagcgctcca 900
ccagcgccgc cgtcctggag gccctccgcg aggcccaccc catcgtggag aagatcctgc 960
agtaccggga gctcaccaag ctgaagagca cctacattga ccccttgccg gacctcatcc 1020
accccaggac gggccgcctc cacacccgct tcaaccagac ggccacggcc acgggcaggc 1080
taagtagctc cgatcccaac ctccagaaca tccccgtccg caccccgctt gggcagagga 1140
tccgccgggc cttcatcgcc gaggaggggt ggctattggt ggccctggac tatagccaga 1200
tagagctcag ggtgctggcc cacctctccg cgacgagaa cctgatccgg gtcttccagg 1260
aggggcggga catccacacg gagaccgcca gctggatgtt cggcgtcccc cgggaggccg 1320
tggacccct gatgcgccgg gcggccaaga ccatcaactt cggggtcctc tacggcatgt 1380
cggcccaccg cctctcccag gagctagcca tcccttacga ggaggcccag gccttcattg 1440
agcgctactt tcagagcttc cccaaggtgc gggcctggat tgagaagacc ctggaggagg 1500
gcaggaggcg ggggtacgtg gagaccctct cggccgccg ccgctacgtg ccagacctag 1560
aggcccgggt gaagagcgtg cgggaggcgg ccgagcgcat ggccttcaac atgcccgtcc 1620
agggcaccgc cgccgacctc atgaagctgg ctatggtgaa gctcttcccc aggctggagg 1680
aaatgggggc caggatgctc cttcaggtcc acgacgagct ggtcctcgag gccccaaaag 1740
agagggcgga ggccgtggcc cggctggcca aggaggtcat ggagggggtg tatcccctgg 1800
ccgtgcccct ggaggtggag gtggggatag gggaggactg gctctccgcc aaggagggca 1860
ttgatggccg cggcggaggc gggcatcatc atcatcatca ttaa            1904
```


<210> 10
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
     Sac7d-deltaTaq

<400> 10

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Met Ile Thr Asn Ser Thr Val Lys Val Lys Phe Lys Tyr Lys Gly Glu
 1               5                  10                  15
Glu Lys Glu Val Asp Thr Ser Lys Ile Lys Lys Val Trp Arg Val Gly
            20                  25                  30
Lys Met Val Ser Phe Thr Tyr Asp Asp Asn Gly Lys Thr Gly Arg Gly
        35                  40                  45
Ala Val Ser Glu Lys Asp Ala Pro Lys Glu Leu Leu Asp Met Leu Ala
    50                  55                  60
Arg Ala Glu Arg Glu Lys Lys Gly Gly Gly Val Thr Ser Pro Lys Ala
65                  70                  75                  80
Leu Glu Glu Ala Pro Trp Pro Pro Glu Gly Ala Phe Val Gly Phe
                85                  90                  95
Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu Leu Ala Leu Ala
            100                 105                 110
Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala
        115                 120                 125
Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala Lys Asp Leu Ser
    130                 135                 140
Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro
145                 150                 155                 160
Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly
                165                 170                 175
Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg
            180                 185                 190
Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu
        195                 200                 205
Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val Glu Arg Pro Leu
    210                 215                 220
Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val Arg Leu Asp Val
225                 230                 235                 240
```

```
Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu Glu Ile Ala Arg
            245                     250                     255
Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn
            260                     265                     270
Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Gly Leu Pro
            275                     280                     285
Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala
            290                     295                     300
Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu
305                     310                     315                 320
Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu
            325                     330                     335
Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn
            340                     345                     350
Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu
            355                     360                     365
Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala
            370                     375                     380
Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln
385                     390                     395                 400
Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile
            405                     410                     415
Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp
            420                     425                     430
Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala
            435                     440                     445
Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg
            450                     455                     460
Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile
465                     470                     475                 480
Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys
            485                     490                     495
Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly
            500                     505                     510
Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg
            515                     520                     525
Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala
            530                     535                     540
Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu
545                     550                     555                 560
Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp Glu Leu Val Leu
            565                     570                     575
Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg Leu Ala Lys Glu
            580                     585                     590
Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val
            595                     600                     605
Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly Ile Asp Gly Arg
            610                     615                     620
Gly Gly Gly Gly His His His His His
625                     630
```

<210> 11
<211> 1965
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
     PL-deltaTaq

<220>
<221> CDS
<222> (1)..(1965)
<223> PL-deltaTaq

<400> 11
atgattacga attcgaagaa aaagaaaaag aaaaagcgta agaaacgcaa aaagaaaaag 60
aaaggcggcg gtgtcactag tggcgcaacc gtaaagttca agtacaaagg cgaagaaaaa 120
gaggtagaca tctccaagat caagaaagta tggcgtgtgg gcaagatgat ctccttcacc 180
tacgacgagg gcggtggcaa gaccggccgt ggtgcggtaa gcgaaaagga cgcgccgaag 240
gagctgctgc agatgctgga gaagcagaaa aagggcggcg tgtcaccag tcccaaggcc 300
ctggaggagg cccccctggcc cccgccggaa ggggccttcg tgggctttgt gctttcccgc 360
aaggagccca tgtgggccga tcttctggcc ctggccgccg ccagggggg ccgggtccac 420
cgggcccccg agccttataa agccctcagg gacctgaagg aggcgcgggg gcttctcgcc 480
aaagacctga gcgttctggc cctgagggaa ggccttggcc tcccgcccgg cgacgacccc 540
atgctcctcg cctacctcct ggacccttcc aacaccaccc ccgaggggt ggcccggcgc 600
tacggcgggg agtggacgga ggaggcgggg gagcgggccg cccttccga gaggctcttc 660
gccaacctgt ggggggaggct tgaggggagg gagaggctcc tttggcttta ccgggaggtg 720
gagaggcccc tttccgctgt cctggcccac atggaggcca cggggggtgcg cctggacgtg 780
gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccgag 840
gtcttccgcc tggccggcca cccccttcaac ctcaactccc gggaccagct ggaaagggtc 900
ctctttgacg agctagggct tcccgccatc ggcaagacgg agaagaccgg caagcgctcc 960
accagcgccg ccgtcctgga ggccctccgc gaggcccacc ccatcgtgga gaagatcctg 1020
cagtaccggg agctcaccaa gctgaagagc acctacattg accccttgcc ggacctcatc 1080
caccccagga cgggccgcct ccacacccgc ttcaaccaga cggccacggc cacgggcagg 1140
ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgct tgggcagagg 1200
atccgccggg ccttcatcgc cgaggagggg tggctattgg tggccctgga ctatagccag 1260
atagagctca gggtgctggc ccacctctcc ggcgacgaga acctgatccg ggtcttccag 1320
gaggggcggg acatccacac ggagaccgcc agctggatgt tcggcgtccc ccgggaggcc 1380
gtggaccccc tgatgcgccg ggcggccaag accatcaact cggggtcct ctacggcatg 1440
tcggcccacc gcctctccca ggagctagcc atcccttacg aggaggccca ggccttcatt 1500
gagcgctact ttcagagctt ccccaaggtg cgggcctgga ttgagaagac cctggaggag 1560
ggcaggaggc gggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagaccta 1620
gaggcccggg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgtc 1680
cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag 1740
gaaatggggg ccaggatgct ccttcaggtc cacgacgagc tggtcctcga ggccccaaaa 1800
gagagggcgg aggccgtggc ccggctggcc aaggaggtca tggaggggt gtatccctg 1860
gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccgc caaggagggc 1920
attgatggcc gcggcggagg cgggcatcat catcatcatc attaa 1965

<210> 12
<211> 654
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:fusion protein
      PL-deltaTaq

<400> 12
Met Ile Thr Asn Ser Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg
 1   5   10   15
Lys Lys Lys Lys Lys Gly Gly Gly Val Thr Ser Gly Ala Thr Val Lys
            20   25   30
Phe Lys Tyr Lys Gly Glu Glu Lys Glu Val Asp Ile Ser Lys Ile Lys
        35   40   45
Lys Val Trp Arg Val Gly Lys Met Ile Ser Phe Thr Tyr Asp Glu Gly
    50   55   60
Gly Gly Lys Thr Gly Arg Gly Ala Val Ser Glu Lys Asp Ala Pro Lys
65   70   75   80

13

```
Glu Leu Leu Gln Met Leu Glu Lys Gln Lys Lys Gly Gly Gly Val Thr
                    85              90                  95
Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
                100             105                 110
Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp Leu
                115             120                 125
Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro Glu
        130             135                 140
Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu Ala
145             150                 155                     160
Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro
                165                 170                 175
Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
                180             185                 190
Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu
            195             200             205
Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp
    210             215                 220
Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu Val
225             230                 235                     240
Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly Val
                245             250                 255
Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala Glu
                260             265                 270
Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His Pro
        275             280                 285
Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
    290             295                 300
Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg Ser
305             310             315                     320
Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
                325             330                 335
Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr
        340             345                 350
Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His
        355             360                 365
Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser
    370             375                 380
Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg
385             390                 395                     400
Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu
                405             410                 415
Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp
                420             425                 430
Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu
        435             440                 445
Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu
    450             455                 460
Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met
465             470                 475                     480
Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala
                485             490                 495
Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala
                500             505                 510
Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu
        515             520                 525
Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val
    530             535                 540
Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val
545             550                 555                     560
```

14

```
Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe
              565                 570                 575
Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His Asp
              580                 585                 590
Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala Arg
          595                 600                 605
Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu
      610                 615                 620
Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu Gly
625                 630                 635                 640
Ile Asp Gly Arg Gly Gly Gly Gly His His His His His His
              645                 650
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<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L71F

<400> 13
cctgctctgc cgcttcacgc   20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L71R

<400> 14
gcacagcggc tggctgagga   20

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L18015F

<400> 15
tgacggagga taacgccagc ag   22

<210> 16
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L23474R

<400> 16
gaaagacgat gggtcgctaa tacgc   25

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L18015F

<400> 17
tgacggagga taacgccagc ag   22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L29930R

<400> 18
ggggttggag gtcaatgggt tc   22

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L30350F

<400> 19
cctgctctgc cgcttcacgc   20

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L35121R

<400> 20
cacatggtac agcaagcctg gc   22

<210> 21
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L2089F

<400> 21
cccgtatctg ctgggatact ggc   23

<210> 22
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L7112R

<400> 22
cagcggtgct gactgaatca tgg   23

<210> 23
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L30350F

<400> 23
cctgcctgcc gcttcacgc   19

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer L40547R

<400> 24
ccaatacccg tttcatcgcg gc   22

<210> 25
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
      H-Amelo-Y

<400> 25
ccacctcatc ctgggcacc   19

<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial
      Sequence:primerH-Amelo-YR

<400> 26
gcttgaggcc aaccatcaga gc   22

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
      beta-globin primer Bglbn536F

<400> 27
ggttggccaa tctactccca gg   22

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
      beta-globin primer Bglbn536R

<400> 28
gctcactcag tgtggcaaag   20

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:human
      beta-globin primer Bglbn1408R

<400> 29
gattagcaaa agggcctagc ttgg   24

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:6-His epitope
      tag

<400> 30
His His His His His His
  1   5

<210> 31
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anti-DYKDDDDK
      epitope tag

18

<400> 31
Asp Tyr Lys Asp Asp Asp Asp Lys
  1   5

<210> 32
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

<400> 32
Gly Gly Val Thr
  1

<210> 33
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide linker

<400> 33
Gly Thr Gly Gly Gly Gly
  1   5

<210> 34
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:lysine-rich
      peptide

<400> 34
Asn Ser Lys Lys Lys Lys Lys Lys Lys Arg Lys Lys Arg Lys Lys Lys
  1   5   10   15
Gly Gly Gly Val Thr
              20